

Glu	Ser	Pro	Arg	Tyr	Leu	Tyr	Ile	Ile	Gln	Asn	Leu	Glu	Gly	Pro	Ala
225					230				235						240
Arg	Lys	Ser	Leu	Lys	Arg	Leu	Thr	Gly	Trp	Ala	Asp	Val	Ser	Gly	Val
			245					250						255	
Leu	Ala	Glu	Leu	Lys	Asp	Glu	Lys	Arg	Lys	Leu	Glu	Arg	Glu	Arg	Pro
			260					265					270		
Leu	Ser	Leu	Leu	Gln	Leu	Leu	Gly	Ser	Arg	Thr	His	Arg	Gln	Pro	Leu
			275				280					285			
Ile	Ile	Ala	Val	Val	Leu	Gln	Leu	Ser	Gln	Gln	Leu	Ser	Gly	Ile	Asn
			290				295					300			
Ala	Val	Phe	Tyr	Tyr	Ser	Thr	Ser	Ile	Phe	Glu	Thr	Ala	Gly	Val	Gly
305					310					315					320
Gln	Pro	Ala	Tyr	Ala	Thr	Ile	Gly	Ala	Gly	Val	Val	Asn	Thr	Val	Phe
				325					330					335	
Thr	Leu	Val	Ser	Val	Leu	Leu	Val	Glu	Arg	Ala	Gly	Arg	Arg	Thr	Leu
			340					345					350		
His	Leu	Leu	Gly	Leu	Ala	Gly	Met	Cys	Gly	Cys	Ala	Ile	Leu	Met	Thr
			355				360					365			
Val	Ala	Leu	Leu	Leu	Leu	Glu	Arg	Val	Pro	Ala	Met	Ser	Tyr	Val	Ser
			370			375				380					
Ile	Val	Ala	Ile	Phe	Gly	Phe	Val	Ala	Phe	Phe	Glu	Ile	Gly	Pro	Gly
385					390					395					400
Pro	Ile	Pro	Trp	Phe	Ile	Val	Ala	Glu	Leu	Phe	Ser	Gln	Gly	Pro	Arg
			405					410						415	
Pro	Ala	Ala	Met	Ala	Val	Ala	Gly	Phe	Ser	Asn	Trp	Thr	Ser	Asn	Phe
			420					425					430		
Ile	Ile	Gly	Met	Gly	Phe	Gln	Tyr	Val	Ala	Glu	Ala	Met	Gly	Pro	Tyr
			435				440					445			
Val	Phe	Leu	Leu	Phe	Ala	Val	Leu	Leu	Leu	Gly	Phe	Phe	Ile	Phe	Thr
			450			455				460					
Phe	Leu	Arg	Val	Pro	Glu	Thr	Arg	Gly	Arg	Thr	Phe	Asp	Gln	Ile	Ser
465					470					475					480
Ala	Ala	Phe	His	Arg	Thr	Pro	Ser	Leu	Leu	Glu	Gln	Glu	Val	Lys	Pro
				485				490						495	
Ser	Thr	Glu	Leu	Glu	Tyr	Leu	Gly	Pro	Asp	Glu	Asn	Asp			
			500					505							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Glu	Gln	Gln	Asp	Gln	Ser	Met	Lys	Glu	Gly	Arg	Leu	Thr	Leu	Val
1				5					10					15	
Leu	Ala	Leu	Ala	Thr	Leu	Ile	Ala	Ala	Phe	Gly	Ser	Ser	Phe	Gln	Tyr
			20					25					30		
Gly	Tyr	Asn	Val	Ala	Ala	Val	Asn	Ser	Pro	Ala	Leu	Leu	Met	Gln	Gln
		35					40					45			
Phe	Tyr	Asn	Glu	Thr	Tyr	Tyr	Gly	Arg	Thr	Gly	Glu	Phe	Met	Glu	Asp
		50				55				60					
Phe	Pro	Leu	Thr	Leu	Leu	Trp	Ser	Val	Thr	Val	Ser	Met	Phe	Pro	Phe
					70					75					80
Gly	Gly	Phe	Ile	Gly	Ser	Leu	Leu	Val	Gly	Pro	Leu	Val	Asn	Lys	Phe
				85					90					95	
Gly	Arg	Lys	Gly	Ala	Leu	Leu	Phe	Asn	Asn	Ile	Phe	Ser	Ile	Val	Pro
			100					105					110		



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TGTTTCCTAG TCTTTGCTAC A

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTGTTAAGGC CTTCCATT

18

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Xaa Xaa Gly Phe Gln Xaa Gly Ser Val Thr Gly Thr Leu Val Leu  
1 5 10 15  
Ala Val Leu Ile Ala Ala Leu Gly Ser Phe Gln Tyr Gly Tyr Asn Leu  
20 25 30  
Gly Val Ile Asn Ala Pro Gln Lys Val Ile Glu Ala Phe Tyr Glu Thr  
35 40 45  
Trp Leu Gly Arg Xaa Gly Glu Xaa Pro Ser Val Pro Thr Leu Thr Leu  
50 55 60  
Leu Trp Ser Leu Ser Val Ser Ile Phe Ala Val Gly Gly Met Ile Gly  
65 70 75 80  
Ser Phe Leu Val Gly Xaa Ile Gly Asn Arg Leu Gly Arg Lys Xaa Ala  
85 90 95  
Met Leu Val Asn Asn Val Leu Ala Ile Ala Gly Gly Leu Leu Met Gly  
100 105 110  
Leu Ala Lys Xaa Ala Xaa Ser Phe Glu Met Leu Ile Leu Gly Arg Phe  
115 120 125  
Ile Ile Gly Leu Tyr Cys Gly Leu Ser Ser Gly Val Val Pro Met Tyr  
130 135 140  
Val Gly Glu Ile Ser Pro Thr Ala Leu Arg Gly Ala Leu Gly Thr Leu  
145 150 155 160  
Asn Gln Leu Gly Ile Val Ile Gly Ile Leu Ile Ala Gln Val Leu Gly  
165 170 175  
Leu Asp Ser Leu Leu Gly Asn Glu Ser Leu Trp Pro Leu Leu Leu Gly  
180 185 190  
Leu Thr Gly Val Pro Ala Leu Leu Gln Leu Leu Leu Leu Pro Phe Cys  
195 200 205  
Pro Glu Ser Pro Arg Tyr Leu Leu Ile Asn Lys Asn Glu Glu Ala Arg  
210 215 220  
Ala Lys Lys Ala Leu Gln Arg Leu Arg Gly Thr Ala Asp Val Ser Gln  
225 230 235 240  
Glu Val Ala Glu Met Lys Asp Glu Ser Arg Xaa Met Xaa Ser Glu Lys  
245 250 255